

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/384,959

DATE: 09/09/1999
TIME: 11:23:06

Input Set: I384959.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

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1  <110> APPLICANT: Sasisekharan, Ram
2      Shriver, Zachary
3      Liu, Dongfang
4      Venkataraman, Ganesh
5  <120> TITLE OF INVENTION: Rationally Designed Heparinases Derived
6      from Heparinase I and II
7  <130> FILE REFERENCE: M0656/7046/HCL
8  <140> CURRENT APPLICATION NUMBER: US/09/384,959
9  <141> CURRENT FILING DATE: 1999-08-27
10 <150> EARLIER APPLICATION NUMBER: US 60/098,153
11 <151> EARLIER FILING DATE: 1998-08-27
12 <160> NUMBER OF SEQ ID NOS: 14
13 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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15 <211> LENGTH: 2339
16 <212> TYPE: DNA
17 <213> ORGANISM: Flavobacterium heparinum
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21      atgcccatac cccctaagac ccaccgcgct ttgtatctac gtgagcagca agttcctgac      180
22      ctgaaaaaca ggatgaacga ccctaaactg aaaaaagttt gggccgatat gatcaagatg      240
23      caggaagact ggaagccagc tgatatctct gaagttaaag actttcgttt ttatttttaac      300
24      cagaaagggc ttactgtaag ggttgaacta atggccctga actatctgat gaccaaggat      360
25      ccaaaggtag gacgggaagc catcacttca attattgata cccttgaaac tgcaactttt      420
26      aaaccagcag gtgatatttc gagagggata gtgatatttc gagagggata ggccctgttta      480
27      tgggttacagg ggccattgtg tatgactggg gctacgatca gctgaaacca gaagagaaaa      540
28      cacgttttgt gaaggcattt gtgaggctgg ccaaaatgct cgaatgtggg tatcctccgg      600
29      taaaagacaa gtctattgtt gggcatgctt ccgaatggat gatcatgcgg gacctgcttt      660
30      ctgtagggat tgccatttac gatgaattcc ctgagatgta taacctggct gcggttcgtt      720
31      ttttcaaaga acacctggtt gcccgcaact gggttttatcc ctgcataac taccatcagg      780
32      gtatgtcata cctgaacgta agattttacca acgacctttt tgccctctgg atattagacc      840
33      ggatggggcg tggtaatgtg tttaatccag ggcagcagtt tatcctttat gacgcgatct      900
34      ataaacgccg ccccgatgga cagatttttag cagggtggaga tgtagattat tccaggaaaa      960
35      aacaaaaata ttatacgatg cctgcattgc ttgcaggtag ctattataaa gatgaatacc      1020
36      ttaattacga attcctgaaa gatcccaatg ttgagccaca ttgcaaattg ttogaatttt      1080
37      tatggcgcg aacccagttg ggaagtcgta agcctgatga tttgccactt tccaggtaact      1140
38      caggatcgcc ttttgatggt atgattgccg gtaccggatg ggggtccggaa agtgtgattg      1200
39      cagagatgaa agtcaacgaa tttccttttc ttaaccatca gcatcaggat gcaggagcct      1260
40      tccagatcta ttacaaaggc ccgctggcca tagatgcagg ctggtatata ggttcttcag      1320
41      gaggttataa cagtcgcgac aacaagaact tttttaagcg gactattgca cacaatagct      1380
42      tgctgattta cgatcctaaa gaaactttca gttcgtcggg atatggtgga agtgaccata      1440
43      ccgattttgc tgccaacgat ggtggtcagc ggctgcccgg aaaagggttg attgcacccc      1500
44      gcgaccttaa agaaatgctg gcaggcgatt tcaggaccgg caaaattctt gcccagggct      1560

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PAGE: 2

RAW SEQUENCE LISTING PATENT APPLICATION US/09/384,959

DATE: 09/09/1999
TIME: 11:23:06

Input Set: I384959.RAW

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47      aagttccggc agcgatgac gtttttgaca aggtagtgtc ttccaatcct gattttaaga      1740
48      agttctggtt gttgcacagt attgagcagc ctgaaataaa ggggaatcag attaccataa      1800
49      aacgtacaaa aaacggtgat agtgggatgt tggatgaatac ggctttgctg ccgcatgcgg      1860
50      ccaattcaaa cattacctcc attggcggca agggcaaaga cttctgggtg tttggtacca      1920
51      attataccaa tgatcctaaa ccgggcacgg atgaagcatt ggaacgtgga gaatggcgtg      1980
52      tggaaatcac tccaaaaaag gcagcagccg aagattacta cctgaatgtg atacagattg      2040
53      ccgacaatac acagcaaaaa ttacacgagg tgaagcgtat tgacggtgac aaggttggtg      2100
54      gtgtgcagct tgctgacagg atagttactt ttagcaaaac ttcagaaact gttgatcgtc      2160
55      cctttggctt ttccgttggt ggtaaaggaa cattcaaatt tgtgatgacc gatcttttag      2220
56      cgggtacctg gcaggtgctg aaagacggaa aaatacttta tctgcgctt tctgcaaaag      2280
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58 <210> SEQ ID NO 2

59 <211> LENGTH: 772

60 <212> TYPE: PRT

61 <213> ORGANISM: Flavobacterium heparinum

62 <400> SEQUENCE: 2

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66      20              25              30
67      Trp Lys Asp Val Asp Gly Val Ser Met Pro Ile Pro Pro Lys Thr His
68      35              40              45
69      Pro Arg Leu Tyr Leu Arg Glu Gln Gln Val Pro Asp Leu Lys Asn Arg
70      50              55              60
71      Met Asn Asp Pro Lys Leu Lys Lys Val Trp Ala Asp Met Ile Lys Met
72      65              70              75              80
73      Gln Glu Asp Trp Lys Pro Ala Asp Ile Pro Glu Val Lys Asp Phe Arg
74      85              90              95
75      Phe Tyr Phe Asn Gln Lys Gly Leu Thr Val Arg Val Glu Leu Met Ala
76      100             105             110
77      Leu Asn Tyr Leu Met Thr Lys Asp Pro Lys Val Gly Arg Glu Ala Ile
78      115             120             125
79      Thr Ser Ile Ile Asp Thr Leu Glu Thr Ala Thr Phe Lys Pro Ala Gly
80      130             135             140
81      Asp Ile Ser Arg Gly Ile Gly Leu Phe Met Val Thr Gly Ala Ile Val
82      145             150             155             160
83      Tyr Asp Trp Cys Tyr Asp Gln Leu Lys Pro Glu Glu Lys Thr Arg Phe
84      165             170             175
85      Val Lys Ala Phe Val Arg Leu Ala Lys Met Leu Glu Cys Gly Tyr Pro
86      180             185             190
87      Pro Val Lys Asp Lys Ser Ile Val Gly His Ala Ser Glu Trp Met Ile
88      195             200             205
89      Met Arg Asp Leu Leu Ser Val Gly Ile Ala Ile Tyr Asp Glu Phe Pro
90      210             215             220
91      Glu Met Tyr Asn Leu Ala Ala Gly Arg Phe Phe Lys Glu His Leu Val
92      225             230             235             240
93      Ala Arg Asn Trp Phe Tyr Pro Ser His Asn Tyr His Gln Gly Met Ser
94      245             250             255

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PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/384,959

DATE: 09/09/1999

TIME: 11:23:06

Input Set: I384959.RAW

95	Tyr	Leu	Asn	Val	Arg	Phe	Thr	Asn	Asp	Leu	Phe	Ala	Leu	Trp	Ile	Leu
96				260					265					270		
97	Asp	Arg	Met	Gly	Ala	Gly	Asn	Val	Phe	Asn	Pro	Gly	Gln	Gln	Phe	Ile
98			275					280					285			
99	Leu	Tyr	Asp	Ala	Ile	Tyr	Lys	Arg	Arg	Pro	Asp	Gly	Gln	Ile	Leu	Ala
100		290					295					300				
101	Gly	Gly	Asp	Val	Asp	Tyr	Ser	Arg	Lys	Lys	Pro	Lys	Tyr	Tyr	Thr	Met
102	305					310					315					320
103	Pro	Ala	Leu	Leu	Ala	Gly	Ser	Tyr	Tyr	Lys	Asp	Glu	Tyr	Leu	Asn	Tyr
104				325						330					335	
105	Glu	Phe	Leu	Lys	Asp	Pro	Asn	Val	Glu	Pro	His	Cys	Lys	Leu	Phe	Glu
106			340						345				350			
107	Phe	Leu	Trp	Arg	Asp	Thr	Gln	Leu	Gly	Ser	Arg	Lys	Pro	Asp	Asp	Leu
108		355					360					365				
109	Pro	Leu	Ser	Arg	Tyr	Ser	Gly	Ser	Pro	Phe	Gly	Trp	Met	Ile	Ala	Arg
110		370					375				380					
111	Thr	Gly	Trp	Gly	Pro	Glu	Ser	Val	Ile	Ala	Glu	Met	Lys	Val	Asn	Glu
112	385				390						395					400
113	Tyr	Ser	Phe	Leu	Asn	His	Gln	His	Gln	Asp	Ala	Gly	Ala	Phe	Gln	Ile
114				405					410					415		
115	Tyr	Tyr	Lys	Gly	Pro	Leu	Ala	Ile	Asp	Ala	Gly	Ser	Tyr	Thr	Gly	Ser
116			420						425				430			
117	Ser	Gly	Gly	Tyr	Asn	Ser	Pro	His	Asn	Lys	Asn	Phe	Phe	Lys	Arg	Thr
118		435					440					445				
119	Ile	Ala	His	Asn	Ser	Leu	Leu	Ile	Tyr	Asp	Pro	Lys	Glu	Thr	Phe	Ser
120		450					455				460					
121	Ser	Ser	Gly	Tyr	Gly	Gly	Ser	Asp	His	Thr	Asp	Phe	Ala	Ala	Asn	Asp
122	465				470					475						480
123	Gly	Gly	Gln	Arg	Leu	Pro	Gly	Lys	Gly	Trp	Ile	Ala	Pro	Arg	Asp	Leu
124				485						490					495	
125	Lys	Glu	Met	Leu	Ala	Gly	Asp	Phe	Arg	Thr	Gly	Lys	Ile	Leu	Ala	Gln
126			500						505				510			
127	Gly	Phe	Gly	Pro	Asp	Asn	Gln	Thr	Pro	Asp	Tyr	Thr	Tyr	Leu	Lys	Gly
128		515					520					525				
129	Asp	Ile	Thr	Ala	Ala	Tyr	Ser	Ala	Lys	Val	Lys	Glu	Val	Lys	Arg	Ser
130		530					535					540				
131	Phe	Leu	Phe	Leu	Asn	Leu	Lys	Asp	Ala	Lys	Val	Pro	Ala	Ala	Met	Ile
132	545				550					555						560
133	Val	Phe	Asp	Lys	Val	Val	Ala	Ser	Asn	Pro	Asp	Phe	Lys	Lys	Phe	Trp
134				565					570					575		
135	Leu	Leu	His	Ser	Ile	Glu	Gln	Pro	Glu	Ile	Lys	Gly	Asn	Gln	Ile	Thr
136			580						585				590			
137	Ile	Lys	Arg	Thr	Lys	Asn	Gly	Asp	Ser	Gly	Met	Leu	Val	Asn	Thr	Ala
138		595					600					605				
139	Leu	Leu	Pro	Asp	Ala	Ala	Asn	Ser	Asn	Ile	Thr	Ser	Ile	Gly	Gly	Lys
140		610					615					620				
141	Gly	Lys	Asp	Phe	Trp	Val	Phe	Gly	Thr	Asn	Tyr	Thr	Asn	Asp	Pro	Lys
142	625				630					635						640
143	Pro	Gly	Thr	Asp	Glu	Ala	Leu	Glu	Arg	Gly	Glu	Trp	Arg	Val	Glu	Ile
144				645					650						655	

PAGE: 4

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/384,959

DATE: 09/09/1999
TIME: 11:23:06

Input Set: I384959.RAW

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145      Thr Pro Lys Lys Ala Ala Ala Glu Asp Tyr Tyr Leu Asn Val Ile Gln
146                      660                      665                      670
147      Ile Ala Asp Asn Thr Gln Gln Lys Leu His Glu Val Lys Arg Ile Asp
148                      675                      680                      685
149      Gly Asp Lys Val Val Gly Val Gln Leu Ala Asp Arg Ile Val Thr Phe
150                      690                      695                      700
151      Ser Lys Thr Ser Glu Thr Val Asp Arg Pro Phe Gly Phe Ser Val Val
152      705                      710                      715                      720
153      Gly Lys Gly Thr Phe Lys Phe Val Met Thr Asp Leu Leu Pro Gly Thr
154                      725                      730                      735
155      Trp Gln Val Leu Lys Asp Gly Lys Ile Leu Tyr Pro Ala Leu Ser Ala
156                      740                      745                      750
157      Lys Gly Asp Asp Gly Pro Leu Tyr Phe Glu Gly Thr Glu Gly Thr Tyr
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159      Arg Phe Leu Arg
160                      770
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163      <212> TYPE: DNA
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169      <222> LOCATION: (236)...(1324)
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173      tttccctttc agcgtacttt ttgggtaaat aaccaataaa aactaaagac gg atg aaa      178
174                                          Met Lys
175                                          1
176      aaa caa att cta tat ctg att gta ctt cag caa ctg ttc ctc tgt tcg      226
177      Lys Gln Ile Leu Tyr Leu Ile Val Leu Gln Gln Leu Phe Leu Cys Ser
178                      5                      10                      15
179      gct tac gcc cag caa aaa aaa tcc ggt aac atc cct tac cgg gta aat      274
180      Ala Tyr Ala Gln Gln Lys Lys Ser Gly Asn Ile Pro Tyr Arg Val Asn
181                      20                      25                      30
182      gtg cag gcc gac agt gct aag cag aag gcg att att gac aac aaa tgg      322
183      Val Gln Ala Asp Ser Ala Lys Gln Lys Ala Ile Ile Asp Asn Lys Trp
184                      35                      40                      45                      50
185      gtg gca gta ggc atc aat aaa cct tat gca tta caa tat gac gat aaa      370
186      Val Ala Val Gly Ile Asn Lys Pro Tyr Ala Leu Gln Tyr Asp Asp Lys
187                      55                      60                      65
188      ctg cgc ttt aat gga aaa cca tcc tat cgc ttt gag ctt aaa gcc gaa      418
189      Leu Arg Phe Asn Gly Lys Pro Ser Tyr Arg Phe Glu Leu Lys Ala Glu
190                      70                      75                      80
191      gac aat tcg ctt gaa ggt tat gct gca gga gaa aca aag ggc cgt aca      466
192      Asp Asn Ser Leu Glu Gly Tyr Ala Ala Gly Glu Thr Lys Gly Arg Thr
193                      85                      90                      95
194      gaa ttg tcg tac agc tat gca acc acc aat gat ttt aag aaa ttt ccc      514

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PAGE: 5

RAW SEQUENCE LISTING PATENT APPLICATION US/09/384,959

DATE: 09/09/1999

TIME: 11:23:06

Input Set: I384959.RAW

195	Glu Leu Ser Tyr Ser Tyr Ala Thr Thr Asn Asp Phe Lys Lys Phe Pro	
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197	cca agc gta tac caa aat gcg caa aag cta aaa acc gtt tat cat tac	562
198	Pro Ser Val Tyr Gln Asn Ala Gln Lys Leu Lys Thr Val Tyr His Tyr	
199	115 120 125 130	
200	ggc aaa ggg att tgt gaa cag ggg agc tcc cgc agc tat acc ttt tca	610
201	Gly Lys Gly Ile Cys Glu Gln Gly Ser Ser Arg Ser Tyr Thr Phe Ser	
202	135 140 145	
203	gtg tac ata ccc tcc tcc ttc ccc gac aat gcg act act att ttt gcc	658
204	Val Tyr Ile Pro Ser Ser Phe Pro Asp Asn Ala Thr Thr Ile Phe Ala	
205	150 155 160	
206	caa tgg cat ggt gca ccc agc aga acg ctt gta gct aca cca gag gga	705
207	Gln Trp His Gly Ala Pro Ser Arg Thr Leu Val Ala Thr Pro Glu Gly	
208	165 170 175	
209	gaa att aaa aca ctg agc ata gaa gag ttt ttg gcc tta tac gac cgc	754
210	Glu Ile Lys Thr Leu Ser Ile Glu Glu Phe Leu Ala Leu Tyr Asp Arg	
211	180 185 190	
212	atg atc ttc aaa aaa aat atc gcc cat gat aaa gtt gaa aaa aaa gat	802
213	Met Ile Phe Lys Lys Asn Ile Ala His Asp Lys Val Glu Lys Lys Asp	
214	195 200 205 210	
215	aag gac gga aaa att act tat gta gcc gga aag cca aat ggc tgg aag	850
216	Lys Asp Gly Lys Ile Thr Tyr Val Ala Gly Lys Pro Asn Gly Trp Lys	
217	215 220 225	
218	gta gaa caa ggt ggt tat ccc acg ctg gcc ttt ggt ttt tct aaa ggg	898
219	Val Glu Gln Gly Gly Tyr Pro Thr Leu Ala Phe Gly Phe Ser Lys Gly	
220	230 235 240	
221	tat ttt tac atc aag gca aac tcc gac cgg cag tgg ctt acc gac aaa	946
222	Tyr Phe Tyr Ile Lys Ala Asn Ser Asp Arg Gln Trp Leu Thr Asp Lys	
223	245 250 255	
224	gcc gac cgt aac aat gcc aat ccc gag aat agt gaa gta atg aag ccc	994
225	Ala Asp Arg Asn Asn Ala Asn Pro Glu Asn Ser Glu Val Met Lys Pro	
226	260 265 270	
227	tat tcc tcg gaa tac aaa act tca acc att gcc tat aaa atg ccc ttt	1042
228	Tyr Ser Ser Glu Tyr Lys Thr Ser Thr Ile Ala Tyr Lys Met Pro Phe	
229	275 280 285 290	
230	gcc cag ttc cct aaa gat tgc tgg att act ttt gat gtc gcc ata gac	1090
231	Ala Gln Phe Pro Lys Asp Cys Trp Ile Thr Phe Asp Val Ala Ile Asp	
232	295 300 305	
233	tgg acg aaa tat gga aaa gag gcc aat aca att ttg aaa ccc ggt aag	1138
234	Trp Thr Lys Tyr Gly Lys Glu Ala Asn Thr Ile Leu Lys Pro Gly Lys	
235	310 315 320	
236	ctg gat gtg atg atg act tat acc aag aat aag aaa cca caa aaa gcg	1186
237	Leu Asp Val Met Met Thr Tyr Thr Lys Asn Lys Lys Pro Gln Lys Ala	
238	325 330 335	
239	cat atc gta aac cag cag gaa atc ctg atc gga cgt aac gat gac gat	1234
240	His Ile Val Asn Gln Gln Glu Ile Leu Ile Gly Arg Asn Asp Asp Asp	
241	340 345 350	
242	ggc tat tac ttc aaa ttt gga att tac agg gtc ggt aac agc acg gtc	1282
243	Gly Tyr Tyr Phe Lys Phe Gly Ile Tyr Arg Val Gly Asn Ser Thr Val	
244	355 360 365 370	

PAGE: 6

VERIFICATION SUMMARY
PATENT APPLICATION US/09/384,959

DATE: 09/09/1999
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Input Set: I384959.RAW

Line ? Error/Warning

Original Text

246 W Line data has been corrected

Pro Val Thr Tyr Asn Leu Ser Gly Tyr Ser G

247 W Invalid/Missing Amino Acid Numbering

375

380